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We claim:

1. An array comprising more than one of the genes in any one of Tables 2-5 hybridized to nucleic acids derived from a cell suspected of being abnormal or malignant.
2. The array of claim 1 wherein more than one comprises more than 5 of the genes in any one of Tables 2-5.
3. The array of claim 1 wherein more than one comprises more than 10 of the genes in any one of Tables 2-5.
4. The array of claim 1 wherein more than one comprises more than 11 of the genes in any one of Tables 2-5.
5. The array of claim 1 wherein said cell is from a subject afflicted with, or suspected of having, breast cancer.
6. The array of claim 5 wherein said subject is human.
7. An array comprising more than one of the genes in Tables 1 or 6 hybridized to nucleic acids derived from a cell suspected of being hyperplastic or cancerous.
8. The array of claim 7 wherein more than one comprises more than 5 of the genes in Tables 1 or 6.
9. The array of claim 7 wherein more than one comprises more than 10 of the genes in Tables 1 or 6.

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10. The array of claim 7 wherein more than one comprises more than 11 of the genes in Tables 1 or 6.
11. The array of claim 7 wherein said cell is from a subject afflicted with, or suspected of having, breast cancer.
12. The array of claim 11 wherein said subject is human.
13. An array comprising more than one of the genes in Table 7 hybridized to nucleic acids derived from a DCIS cell.
14. An array comprising more than one of the genes in Table 8 hybridized to nucleic acids derived from a IDC cell.
15. A method to determine the breast cancer stage of a ductal lavage or fine needle aspiration sample from a subject comprising assaying said sample for expression of one or more genes correlated with one or more stages of breast cancer.
16. The method of claim 15 wherein said assaying comprises preparing RNA from said sample.
17. The method of claim 14 wherein said RNA is amplified.
18. The method of claim 15 wherein said assaying comprises using an array.
19. The method of claim 15 wherein said assaying comprises using the array of claim 1.

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18. The method of claim 15 wherein said one or more genes are correlated with ADH, DCIS, and/or IDC.

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19. The method of claim 15 wherein said one or more genes are correlated with normal and abnormal cells.

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20. A method to determine breast cancer stage of a cell containing sample from a subject comprising assaying said sample for expression of one or more genes capable of discriminating between two stages of breast cancer.

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21. The method of claim 20 wherein said sample is from a subject afflicted with, or suspected of having, breast cancer.

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22. The method of claim 20 wherein said subject is human.

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23. The method of claim 20 wherein said sample is a microdissected sample.

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24. The method of claim 23 wherein said sample is microdissected via laser capture microdissection.

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25. The method of claim 20 wherein said one or more genes discriminate between normal and abnormal cells, between cancerous and non-cancerous cells, or between stages of DCIS or IDC.

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26. A method to determine therapeutic treatment for a patient determined to have atypical cells in a sample therefrom comprising

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assaying said cells for expression of genes correlated with non-cancerous and cancerous breast cancer cells, identifying the stage of breast cancer of said cells, and selecting the appropriate treatment for a patient having cells of such a stage.

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27.

A method to identify genes the expression of which are correlated with one or more stages of breast cancer comprising

obtaining multiple homogenous populations of breast cancer cells from each of said one or more stages;

identifying more than one gene the expression of which is correlated with said one or more stage by detecting genes with similar expression profiles in more than one of said populations.

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